

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/090,867

DATE: 06/15/98
TIME: 12:20:06

INPUT SET: S26648.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Baumgartner, James W.
6 Farrah, Theresa M.
7 Foster, Donald C.
8 Grant, Frank J.
9 O'Hara, Patrick J.
10
11 (ii) TITLE OF INVENTION: Testis-Specific Receptor
12
13 (iii) NUMBER OF SEQUENCES: 33
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: ZymoGenetics, Inc.
17 (B) STREET: 1201 Eastlake Avenue East
18 (C) CITY: Seattle
19 (D) STATE: WA
20 (E) COUNTRY: USA
21 (F) ZIP: 98102
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Parker, Gary E.
36 (B) REGISTRATION NUMBER: 31,648
37 (C) REFERENCE/DOCKET NUMBER: 95-33
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 206-442-6673
41 (B) TELEFAX: 206-442-6678
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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DATE: 06/15/98
TIME: 12:20:07

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47      (A) LENGTH: 1289 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: double
50      (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 49..1191
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      CCCCCCGCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC      57
63                                         Met Ala Phe
64                                         1
65
66      GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA      105
67      Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr
68          5                      10                      15
69
70      TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT      153
71      Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro
72          20                      25                      30                      35
73
74      CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG      201
75      Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu
76          40                      45                      50
77
78      CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG      249
79      Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val
80          55                      60                      65
81
82      GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC      297
83      Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr
84          70                      75                      80
85
86      ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG      345
87      Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys
88          85                      90                      95
89
90      GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT      393
91      Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn
92      100                      105                      110                      115
93
94      GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA      441
95      Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser
96          120                      125                      130
97
98      CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT      489
99      Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr

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100		135		140		145	
101							
102	TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA						537
103	Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val						
104	150		155		160		
105							
106	CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT						585
107	Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp						
108	165		170		175		
109							
110	CAT GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA						633
111	His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile						
112	180		185		190		195
113							
114	GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT						681
115	Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr						
116	200		205		210		
117							
118	ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT						729
119	Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr						
120	215		220		225		
121							
122	TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT						777
123	Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr						
124	230		235		240		
125							
126	CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC						825
127	Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser						
128	245		250		255		
129							
130	ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG						873
131	Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu						
132	260		265		270		275
133							
134							
135							
136	ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA						921
137	Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu						
138	280		285		290		
139							
140	ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA						969
141	Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val						
142	295		300		305		
143							
144	GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT						1017
145	Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser						
146	310		315		320		
147							
148	GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA						1065
149	Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys						
150	325		330		335		
151							
152	ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT						1113

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153 Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val
154 340 345 350 355
155
156 ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA 1161
157 Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys
158 360 365 370
159
160 ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG 1208
161 Met Ile Pro Glu Phe Phe Cys Asp Thr
162 375 380
163
164 AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTCATAT GAGTCTCAAT 1268
165
166 AAACTGAATT TTTCTTGCGA A 1289
167
168
169 (2) INFORMATION FOR SEQ ID NO:2:
170
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 380 amino acids
173 (B) TYPE: amino acid
174 (D) TOPOLOGY: linear
175
176 (ii) MOLECULE TYPE: protein
177
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
179
180
181
182 Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
183 1 5 10 15
184
185 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
186 20 25 30
187
188 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
189 35 40 45
190
191 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
192 50 55 60
193
194 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
195 65 70 75 80
196
197 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
198 85 90 95
199
200 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
201 100 105 110
202
203 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
204 115 120 125
205

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206  Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
207      130                      135                      140
208
209  Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
210      145                      150                      155                      160
211
212  Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
213                      165                      170                      175
214
215  Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
216                      180                      185                      190
217
218  Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
219                      195                      200                      205
220
221  Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
222      210                      215                      220
223
224  Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225      225                      230                      235                      240
226
227  Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
228                      245                      250                      255
229
230  Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
231                      260                      265                      270
232
233  Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
234      275                      280                      285
235
236  Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
237      290                      295                      300
238
239  Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
240      305                      310                      315                      320
241
242  Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
243                      325                      330                      335
244
245  Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
246      340                      345                      350
247
248  Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
249      355                      360                      365
250
251  Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
252      370                      375                      380
253
254

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1167 base pairs

RAW SEQUENCE LISTING PATENT APPLICATION US/09/090,867

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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

255 (2) INFORMATION FOR SEQ ID NO:3:

256

257 (i) SEQUENCE CHARACTERISTICS:

258 (A) LENGTH: 1167 base pairs

259 (B) TYPE: nucleic acid

260 (C) STRANDEDNESS: double

261 (D) TOPOLOGY: linear

262

263 (ii) MOLECULE TYPE: cDNA

264

265

266 (ix) FEATURE:

267 (A) NAME/KEY: CDS

268 (B) LOCATION: 10..1152

269

270

271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

272

273 GATCCGCCC ATG GCT TTC GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC 48

274 Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr

275 1 5 10

276

277 TTT CTG ATA AGC ACA ACA TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG 96

278 Phe Leu Ile Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu

279 15 20 25

280

281 ATA AAA GTT AAC CCT CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC 144

282 Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr

283 30 35 40 45

284

285 TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT 192

286 Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His

287 50 55 60

288

289 TTT AAG GAA TAC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT 240

290 Phe Lys Glu Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly

291 65 70 75

292

293 AGT GAA ACA TGG AAG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT 288

294 Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp

295 80 85 90

296

297 GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA 336

298 Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu

299 95 100 105

300

301 CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA 384

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302	Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	
303	110					115					120					125	
304																	
305	ACT	ACT	TAT	TGG	ATA	TCA	CCA	CAA	GGA	ATT	CCA	GAA	ACT	AAA	GTT	CAG	432
306	Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	
307					130					135					140		
308																	
309	GAT	ATG	GAT	TGC	GTA	TAT	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	480
310	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	
311				145					150					155			
312																	
313	AAA	CCT	GGC	ATA	GGT	GTA	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	528
314	Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	
315			160					165					170				
316																	
317	TGG	TAT	GAG	GGC	TTG	GAT	CTT	GCA	TTA	CAG	TGT	GTT	GAT	TAC	ATC	AAG	576
318	Trp	Tyr	Glu	Gly	Leu	Asp	Leu	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	
319		175					180					185					
320																	
321	GCT	GAT	GGA	CAA	AAT	ATA	GGA	TGC	AGA	TTT	CCC	TAT	TTG	GAG	GCA	TCA	624
322	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	
323	190				195					200						205	
324																	
325	GAC	TAT	AAA	GAT	TTC	TAT	ATT	TGT	GTT	AAT	GGA	TCA	TCA	GAG	AAC	AAG	672
326	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Asn	Lys	
327					210					215				220			
328																	
329	CCT	ATC	AGA	TCC	AGT	TAT	TTC	ACT	TTT	CAG	CTT	CAA	AAT	ATA	GTT	AAA	720
330	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	
331				225					230					235			
332																	
333	CCT	TTG	CCG	CCA	GTC	TAT	CTT	ACT	TTT	ACT	CGG	GAG	AGT	TCA	TGT	GAA	768
334	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	
335			240					245				250					
336																	
337	ATT	AAG	CTG	AAA	TGG	GGC	ATA	CCT	TTG	GGA	CCT	ATT	CCA	GCA	AGG	TGT	816
338	Ile	Lys	Leu	Lys	Trp	Gly	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	
339		255					260					265					
340																	
341	TTT	GAT	TAT	GAA	ATT	GAG	ATC	AGA	GAA	GAT	GAT	ACT	ACC	TTG	GTG	ACT	864
342	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	
343	270					275					280				285		
344																	
345	GCT	ACA	GTT	GAA	AAT	GAA	ACA	TAC	ACC	TTG	AAA	ACA	ACA	AAT	GAA	ACC	912
346	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	
347					290					295				300			
348																	
349	CGA	CAA	TTA	TGC	TTT	GTA	GTA	AGA	AGC	AAA	GTG	AAT	ATT	TAT	TGC	TCA	960
350	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	
351				305					310					315			
352																	
353	GAT	GAC	GGA	ATT	TGG	AGT	GAG	TGG	AGT	GAT	AAA	CAA	TGC	TGG	GAA	GGT	1008
354	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	

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355	320				325				330								
356																	
357	GAA	GAC	CTA	TCG	AAG	AAA	ACT	TTG	CTA	CGT	TTC	TGG	CTA	CCA	TTT	GGT	1056
358	Glu	Asp	Leu	Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	
359	335				340				345								
360																	
361																	
362																	
363	TTC	ATC	TTA	ATA	TTA	GTT	ATA	TTT	GTA	ACC	GGT	CTG	CTT	TTG	CGT	AAG	1104
364	Phe	Ile	Leu	Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	
365	350				355				360				365				
366																	
367	CCA	AAC	ACC	TAC	CCA	AAA	ATG	ATT	CCA	GAA	TTT	TTC	TGT	GAT	ACA	TGAAGACTTT	1159
368	Pro	Asn	Thr	Tyr	Pro	Lys	Met	Ile	Pro	Glu	Phe	Phe	Cys	Asp	Thr		
369	370				375				380								
370																	
371	CCTCTAGA																1167
372																	
373																	

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